ENTERED

$p.5$

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     RAW SEQUENCE LISTING              DATE: 10/04/2001
     PATENT APPLICATION:  US/09/737,246    TIME: 17:18:13

     Input Set : A:\-3-1-1.app
     Output Set: N:\CRF3\10042001\I737246.raw


  3 <110> APPLICANT: Lu, Peter
  4        Garman, Jonathan David
  5        Candia III, Albert Frederick
  6        Arbor Vita Corporation
  8 <120> TITLE OF INVENTION: CLASP-3 Transmembrane Protein
 10 <130> FILE REFERENCE: 020054-000311US
 12 <140> CURRENT APPLICATION NUMBER: US 09/737,246
C--> 13 <141> CURRENT FILING DATE: 2001-09-20
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 16 <151> PRIOR FILING DATE: 1999-10-21
 18 <150> PRIOR APPLICATION NUMBER: US 60/162,498
 19 <151> PRIOR FILING DATE: 1999-10-29
 21 <150> PRIOR APPLICATION NUMBER: US 60/170,453
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 31 <151> PRIOR FILING DATE: 2000-04-11
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 42 <150> PRIOR APPLICATION NUMBER: US 60/196,528
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 45 <150> PRIOR APPLICATION NUMBER: US 09/687,837
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 48 <150> PRIOR APPLICATION NUMBER: US 60/240,503
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 57 <150> PRIOR APPLICATION NUMBER: US 60/240,543
 58 <151> PRIOR FILING DATE: 2000-10-13
 60 <160> NUMBER OF SEQ ID NOS: 148
 62 <170> SOFTWARE: PatentIn Ver. 2.1
 64 <210> SEQ ID NO: 1
 65 <211> LENGTH: 6828
 66 <212> TYPE: DNA
 67 <213> ORGANISM: Homo sapiens
 69 <220> FEATURE:
 70 <223> OTHER INFORMATION: full-length human CLASP-3 cDNA
 72 <220> FEATURE:
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RAW SEQUENCE LISTING   DATE: 10/04/2001
PATENT APPLICATION: US/09/737,246   TIME: 17:18:13

Input Set : A:\-3-1-1.app
Output Set: N:\CRF3\10042001\I737246.raw

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74 <222> LOCATION: (22)..(6294)
75 <223> OTHER INFORMATION: human CLASP-3

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82 atc agc aga acg gtg gca gcc gaa gtt agg aag cag atc tcc gga caa    99
83 Ile Ser Arg Thr Val Ala Ala Glu Val Arg Lys Gln Ile Ser Gly Gln
84              15                  20                  25
86 tat agt ggt tct ccc caa ctg ctc aaa aac ctt aat att gtt ggc aat   147
87 Tyr Ser Gly Ser Pro Gln Leu Leu Lys Asn Leu Asn Ile Val Gly Asn
88              30                  35                  40
90 ata tcc cat cac acc aca gtg ccc ctt acc gaa gca gta gat cca gtg   195
91 Ile Ser His His Thr Thr Val Pro Leu Thr Glu Ala Val Asp Pro Val
92          45                  50                  55
94 gat ttg gaa gat tac ctc att act cat cct ttg gct gtg gat tct ggg   243
95 Asp Leu Glu Asp Tyr Leu Ile Thr His Pro Leu Ala Val Asp Ser Gly
96      60                  65                  70
98 cct tta cgg gat ttg att gaa ttt cct cca gat gat att gaa gtt gtt   291
99 Pro Leu Arg Asp Leu Ile Glu Phe Pro Pro Asp Asp Ile Glu Val Val
100  75                  80                  85                  90
102 tat agt cct cgg gac tgc aga act ctt gtt tca gct gta cct gaa gaa  339
103 Tyr Ser Pro Arg Asp Cys Arg Thr Leu Val Ser Ala Val Pro Glu Glu
104              95                 100                 105
106 agt gaa atg gat cca cat gtt aga gac tgt ata aga agt tat aca gaa  387
107 Ser Glu Met Asp Pro His Val Arg Asp Cys Ile Arg Ser Tyr Thr Glu
108             110                 115                 120
110 gac tgg gca att gtc atc aga aaa tat cat aaa ttg gga aca gga ttt  435
111 Asp Trp Ala Ile Val Ile Arg Lys Tyr His Lys Leu Gly Thr Gly Phe
112         125                 130                 135
114 aat ccc aat aca tta gat aaa cag aaa gaa agg caa aaa ggt ttg cca  483
115 Asn Pro Asn Thr Leu Asp Lys Gln Lys Glu Arg Gln Lys Gly Leu Pro
116     140                 145                 150
118 aaa caa gtt ttt gaa tct gat gaa gct cca gat ggc aac agc tac cag  531
119 Lys Gln Val Phe Glu Ser Asp Glu Ala Pro Asp Gly Asn Ser Tyr Gln
120 155                 160                 165                 170
122 gat gat caa gat gac ctt aaa aga cgt tca atg tca ata gat gat acc  579
123 Asp Asp Gln Asp Asp Leu Lys Arg Arg Ser Met Ser Ile Asp Asp Thr
124             175                 180                 185
126 cca agg ggt agc tgg gcc tgt agt atc ttt gac ttg aaa aat tca ctt  627
127 Pro Arg Gly Ser Trp Ala Cys Ser Ile Phe Asp Leu Lys Asn Ser Leu
128             190                 195                 200
130 cct gat gct ttg ctt ccc aat tta ctt gat cga act cca aat gaa gaa  675
131 Pro Asp Ala Leu Leu Pro Asn Leu Leu Asp Arg Thr Pro Asn Glu Glu
132         205                 210                 215
134 ata gac cgt cag aat gat gac caa agg aaa tca aac cgt cac aaa gaa  723
135 Ile Asp Arg Gln Asn Asp Asp Gln Arg Lys Ser Asn Arg His Lys Glu
136         220                 225                 230
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RAW SEQUENCE LISTING   DATE: 10/04/2001
PATENT APPLICATION: US/09/737,246   TIME: 17:18:13

Input Set : A:\-3-1-1.app
Output Set: N:\CRF3\10042001\I737246.raw

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139 Leu Phe Ala Leu His Pro Ser Pro Asp Glu Glu Glu Pro Ile Glu Arg
140 235                 240                 245                 250
142 ctt agt gtt cct gat ata ccc aaa gaa cat ttt ggt caa aga ctt ctt   819
143 Leu Ser Val Pro Asp Ile Pro Lys Glu His Phe Gly Gln Arg Leu Leu
144                     255                 260                 265
146 gta aaa tgc tta tca ctc aag ttt gaa att gaa att gaa ccc att ttt   867
147 Val Lys Cys Leu Ser Leu Lys Phe Glu Ile Glu Ile Glu Pro Ile Phe
148                 270                 275                 280
150 gca agt ttg gct tta tat gat gtc aag gaa aag aaa aag att tca gaa   915
151 Ala Ser Leu Ala Leu Tyr Asp Val Lys Glu Lys Lys Lys Ile Ser Glu
152             285                 290                 295
154 aac ttt tat ttt gac ctt aat tct gag cag atg aaa ggg ttg tta cgt   963
155 Asn Phe Tyr Phe Asp Leu Asn Ser Glu Gln Met Lys Gly Leu Leu Arg
156     300                 305                 310
158 cca cat gta cca cct gct gcc att act acc ctg gca aga tca gca att   1011
159 Pro His Val Pro Pro Ala Ala Ile Thr Thr Leu Ala Arg Ser Ala Ile
160 315                 320                 325                 330
162 ttt tct atc act tat cct tcc caa gat gtt ttt ctt gta ata aag cta   1059
163 Phe Ser Ile Thr Tyr Pro Ser Gln Asp Val Phe Leu Val Ile Lys Leu
164                 335                 340                 345
166 gaa aaa gtc cta cag caa gga gac att gga gag tgt gca gaa cca tat   1107
167 Glu Lys Val Leu Gln Gln Gly Asp Ile Gly Glu Cys Ala Glu Pro Tyr
168             350                 355                 360
170 atg att ttc aaa gaa gca gat gcc acc aag aat aaa gaa aaa ctg gag   1155
171 Met Ile Phe Lys Glu Ala Asp Ala Thr Lys Asn Lys Glu Lys Leu Glu
172         365                 370                 375
174 aaa ctg aag agt caa gca gat cag ttt tgc caa aga ctt ggg aaa tat   1203
175 Lys Leu Lys Ser Gln Ala Asp Gln Phe Cys Gln Arg Leu Gly Lys Tyr
176     380                 385                 390
178 cgc atg cct ttt gct tgg act gca atc cat tta atg aat att gtt agc   1251
179 Arg Met Pro Phe Ala Trp Thr Ala Ile His Leu Met Asn Ile Val Ser
180 395                 400                 405                 410
182 agt gct ggg agt ttg gaa aga gat tct aca gaa gta gaa atc agt act   1299
183 Ser Ala Gly Ser Leu Glu Arg Asp Ser Thr Glu Val Glu Ile Ser Thr
184                 415                 420                 425
186 gga gaa cga aaa ggg tct tgg tca gag agg agg aat tct agt att gtt   1347
187 Gly Glu Arg Lys Gly Ser Trp Ser Glu Arg Arg Asn Ser Ser Ile Val
188             430                 435                 440
190 ggc aga cga tca ctt gaa agg aca aca agt gga gat gat gct tgt aac   1395
191 Gly Arg Arg Ser Leu Glu Arg Thr Thr Ser Gly Asp Asp Ala Cys Asn
192         445                 450                 455
194 ttg acg agc ttt cga cca gct act ctc aca gtg aca aat ttt ttt aag   1443
195 Leu Thr Ser Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys
196     460                 465                 470
198 cag gaa gga gac cgc tta agt gat gaa gat ctc tac aaa ttc ctt gct   1491
199 Gln Glu Gly Asp Arg Leu Ser Asp Glu Asp Leu Tyr Lys Phe Leu Ala
200 475                 480                 485                 490
202 gat atg aga agg cca tct tct gtc tta cgg cga cta aga cct att aca   1539
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203 Asp Met Arg Arg Pro Ser Ser Val Leu Arg Arg Leu Arg Pro Ile Thr
204             495             500             505
206 gct cag ctc aag ata gac att tct ccc gca cct gaa aat ccc cat tat  1587
207 Ala Gln Leu Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Tyr
208             510             515             520
210 tgc cta act ccg gag ctg ctt caa gtg aag ctt tac cct gac agt aga  1635
211 Cys Leu Thr Pro Glu Leu Leu Gln Val Lys Leu Tyr Pro Asp Ser Arg
212             525             530             535
214 gtt aga cct acc aga gaa atc tta gag ttt ccc gca agg gat gtt tat  1683
215 Val Arg Pro Thr Arg Glu Ile Leu Glu Phe Pro Ala Arg Asp Val Tyr
216     540             545             550
218 gtt cca aac act act tac aga aat ctt ctc tac ata tac cct cag agt  1731
219 Val Pro Asn Thr Thr Tyr Arg Asn Leu Leu Tyr Ile Tyr Pro Gln Ser
220 555             560             565             570
222 ctt aat ttt gcc aat cgt caa ggt tct gct aga aat ata aca gtg aaa  1779
223 Leu Asn Phe Ala Asn Arg Gln Gly Ser Ala Arg Asn Ile Thr Val Lys
224             575             580             585
226 gtc cag ttt atg tat gga gag gat cca agc aat gcc atg ccg gta atc  1827
227 Val Gln Phe Met Tyr Gly Glu Asp Pro Ser Asn Ala Met Pro Val Ile
228             590             595             600
230 ttt ggt aaa tct agc tgt tca gaa ttt tca aag gaa gcc tat aca gcc  1875
231 Phe Gly Lys Ser Ser Cys Ser Glu Phe Ser Lys Glu Ala Tyr Thr Ala
232             605             610             615
234 gta gta tat cat aac agg tct cct gat ttt cat gaa gaa atc aag gtt  1923
235 Val Val Tyr His Asn Arg Ser Pro Asp Phe His Glu Glu Ile Lys Val
236     620             625             630
238 aag ctt cct gct act tta act gac cat cat cac ttg ctt ttt act ttt  1971
239 Lys Leu Pro Ala Thr Leu Thr Asp His His His Leu Leu Phe Thr Phe
240 635             640             645             650
242 tat cat gtt agt tgt caa caa aaa caa aat act cct ctt gaa aca cca  2019
243 Tyr His Val Ser Cys Gln Gln Lys Gln Asn Thr Pro Leu Glu Thr Pro
244             655             660             665
246 gtt gga tat aca tgg ata cca atg ctt cag aat gga cgg ttg aag act  2067
247 Val Gly Tyr Thr Trp Ile Pro Met Leu Gln Asn Gly Arg Leu Lys Thr
248             670             675             680
250 ggc cag ttt tgc ttg cca gtc tca ttg gaa aaa cca cca cag gct tat  2115
251 Gly Gln Phe Cys Leu Pro Val Ser Leu Glu Lys Pro Pro Gln Ala Tyr
252             685             690             695
254 tct gta ctg tct cct gag gtt cct cta cct ggc atg aaa tgg gta gat  2163
255 Ser Val Leu Ser Pro Glu Val Pro Leu Pro Gly Met Lys Trp Val Asp
256     700             705             710
258 aat cac aaa ggt gtt ttt aat gtt gaa gtt gtt gct gtt tcg tct atc  2211
259 Asn His Lys Gly Val Phe Asn Val Glu Val Val Ala Val Ser Ser Ile
260 715             720             725             730
262 cat aca caa gat cct tat ctt gac aaa ttt ttt gct ctg gtc aat gct  2259
263 His Thr Gln Asp Pro Tyr Leu Asp Lys Phe Phe Ala Leu Val Asn Ala
264             735             740             745
266 ctg gat gaa cac ctg ttc cca gtc cga att ggg gac atg cga atc atg  2307
267 Leu Asp Glu His Leu Phe Pro Val Arg Ile Gly Asp Met Arg Ile Met
```

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268            750              755              760
270 gaa aat aac tta gaa aat gaa ttg aag agc agt att tca gca ctg aat    2355
271 Glu Asn Asn Leu Glu Asn Glu Leu Lys Ser Ser Ile Ser Ala Leu Asn
272            765              770              775
274 tca tcc cag ctg gaa cca gtg gtc cga ttt ctt cat ctt ctg cta gat    2403
275 Ser Ser Gln Leu Glu Pro Val Val Arg Phe Leu His Leu Leu Leu Asp
276        780              785              790
278 aaa ctg ata ctt tta gtt att aga cct cct gtc att gct ggc caa ata    2451
279 Lys Leu Ile Leu Leu Val Ile Arg Pro Pro Val Ile Ala Gly Gln Ile
280 795              800              805              810
282 gtt aac cta ggt caa gca tct ttt gaa gcc atg gca tca att ata aat    2499
283 Val Asn Leu Gly Gln Ala Ser Phe Glu Ala Met Ala Ser Ile Ile Asn
284            815              820              825
286 cga ctt cac aaa aac ttg gaa gga aat cat gac cag cat ggc aga aac    2547
287 Arg Leu His Lys Asn Leu Glu Gly Asn His Asp Gln His Gly Arg Asn
288            830              835              840
290 agc ctt ctt gca tca tat att cat tat gtt ttc cgc cta cca aat act    2595
291 Ser Leu Leu Ala Ser Tyr Ile His Tyr Val Phe Arg Leu Pro Asn Thr
292        845              850              855
294 tac cct aat tca tca tca cca ggt cct ggg ggt ttg gga gga tca gtg    2643
295 Tyr Pro Asn Ser Ser Ser Pro Gly Pro Gly Gly Leu Gly Gly Ser Val
296        860              865              870
298 cat tat gcc aca atg gct aga tct gcg gtg aga cct gca agc ctt aat    2691
299 His Tyr Ala Thr Met Ala Arg Ser Ala Val Arg Pro Ala Ser Leu Asn
300 875              880              885              890
302 tta aat cgt tct cga agc ctt agt aat agc aat cca gat ata tct ggg    2739
303 Leu Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp Ile Ser Gly
304            895              900              905
306 act ccc acg tca cca gat gat gaa gtt cga tca atc atc ggg agt aag    2787
307 Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile Gly Ser Lys
308            910              915              920
310 ggt tta gat cgc tcc aat tcc tgg gtt aac act ggt ggt cca aaa gct    2835
311 Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly Pro Lys Ala
312        925              930              935
314 gcc cca tgg gga tcc aac ccc agt cca agt gca gaa tca aca cag gct    2883
315 Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser Thr Gln Ala
316        940              945              950
318 atg gat cga agt tgt aat cgt atg tct tcg cac aca gag acg tca agt    2931
319 Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu Thr Ser Ser
320 955              960              965              970
322 ttc tta caa aca tta acg gga cgc tta cca act aaa aag ctt ttt cac    2979
323 Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys Leu Phe His
324            975              980              985
326 gag gag ctg gct ttg cag tgg gtt gtt tgc agt ggc agc gtt cgg gaa    3027
327 Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser Val Arg Glu
328            990              995              1000
330 tca gct ttg caa caa gcc tgg ttc ttt ttt gaa tta atg gta aag agc    3075
331 Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu Met Val Lys Ser
332            1005             1010             1015
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VERIFICATION SUMMARY   DATE: 10/04/2001
PATENT APPLICATION: US/09/737,246   TIME: 17:18:14

Input Set : A:\-3-1-1.app
Output Set: N:\CRF3\10042001\I737246.raw

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L:1041 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:1047 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:
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L:4726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:4727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:4728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:4753 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:4755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
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VERIFICATION SUMMARY   DATE: 10/04/2001
PATENT APPLICATION: **US/09/737,246**   TIME: 17:18:14

Input Set : **A:\-3-1-1.app**
Output Set: **N:\CRF3\10042001\I737246.raw**

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L:4913 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
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L:8040 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (107) SEQUENCE:
L:8046 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (108) SEQUENCE:
L:8052 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (109) SEQUENCE:
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L:8082 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (114) SEQUENCE:
L:8088 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (115) SEQUENCE:
L:8094 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (116) SEQUENCE:
L:8100 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (117) SEQUENCE:
L:8106 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (118) SEQUENCE:
L:8112 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (119) SEQUENCE:
L:8118 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (120) SEQUENCE:
L:8124 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (121) SEQUENCE:
L:8130 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (122) SEQUENCE:
L:8136 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (123) SEQUENCE:
L:8142 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (124) SEQUENCE:
L:8148 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (125) SEQUENCE:
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